

THAT WHICH IS CLAIMED:

1. An isolated nucleic acid molecule having a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence encoding a fragment of the amino acid sequence set forth in SEQ ID NO:1, wherein said nucleotide sequence comprises at least 500 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:2 and said fragment has aminopeptidase activity;

(b) a nucleotide sequence encoding a fragment of the amino acid sequence encoded by the cDNA insert contained in the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said nucleotide sequence comprises at least 500 contiguous nucleotides of the nucleotide sequence of the cDNA insert of the plasmid deposited with ATCC as Patent Deposit No. PTA-2811 and said fragment has aminopeptidase activity; and

(c) a nucleotide sequence complementary to at least one of the nucleotide sequences in (a) or (b).

2. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence encoding a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said nucleotide sequence has at least about 85% sequence identity with the nucleotide sequence set forth in SEQ ID NO:2, and said sequence variant has aminopeptidase activity;

(b) a nucleotide sequence encoding a sequence variant of the amino acid sequenced encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said nucleotide sequence has at least about 85% sequence identity with the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811 and said sequence variant has aminopeptidase activity;

(c) a nucleotide sequence encoding a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said nucleotide sequence has at least about 90% sequence identity with the nucleotide sequence set forth in SEQ ID NO:2, and said sequence variant has aminopeptidase activity;

(d) a nucleotide sequence encoding a sequence variant of the amino acid sequenced encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said nucleotide sequence has at least about 90% sequence identity with the cDNA insert of the plasmid deposited with the ATCC as

5 Patent Deposit No. PTA-2811 and said sequence variant has aminopeptidase activity;

(e) a nucleotide sequence encoding a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said nucleotide sequence has at least about 95% sequence identity with the nucleotide sequence set forth in SEQ ID NO:2, and said sequence variant has aminopeptidase activity;

10 (f) a nucleotide sequence encoding a sequence variant of the amino acid sequenced encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said nucleotide sequence has at least about 95% sequence identity with the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811 and said sequence variant has aminopeptidase activity; and

15 (g) a nucleotide sequence complementary to at least one of the nucleotide sequences in (a), (b), (c), (d), (e), or (f); wherein said sequence identity is calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4.

20 3. The isolated nucleic acid molecule of claim 2, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group

(a) a nucleotide sequence encoding a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said nucleotide sequence has at least about 85% sequence identity with the nucleotide sequence set forth in SEQ ID NO:2, and
25 said sequence variant has aminopeptidase activity;

(b) a nucleotide sequence encoding a sequence variant of the amino acid sequenced encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said nucleotide sequence has at least about 85% sequence identity with the cDNA insert of the plasmid deposited with the ATCC as
30 Patent Deposit No. PTA-2811, and said sequence variant has aminopeptidase activity; and

(c) a nucleotide sequence complementary to at least one of the nucleotide sequences of (a) or (b); wherein said sequence identity is calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4.

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4. The isolated nucleic acid molecule of claim 3, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group

(a) a nucleotide sequence encoding a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said nucleotide sequence has at least about 90% sequence identity with the nucleotide sequence set forth in SEQ ID NO:2, and said sequence variant has aminopeptidase activity;

(b) a nucleotide sequence encoding a sequence variant of the amino acid sequenced encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said nucleotide sequence has at least about 90% sequence identity with the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, and said sequence variant has aminopeptidase activity; and

(c) a nucleotide sequence complementary to at least one of the nucleotide sequences of (a) or (b); wherein said sequence identity is calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4.

5. The isolated nucleic acid molecule of claim 4, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group

(a) a nucleotide sequence encoding a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said nucleotide sequence has at least about 95% sequence identity with the nucleotide sequence set forth in SEQ ID NO:2, and said sequence variant has aminopeptidase activity;

(b) a nucleotide sequence encoding a sequence variant of the amino acid sequenced encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said nucleotide sequence has at least about 95%

sequence identity with the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, and said sequence variant has aminopeptidase activity; and

- 5 (c) a nucleotide sequence complementary to at least one of the nucleotide sequences of (a) or (b); wherein said sequence identity is calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4.

6. A method for producing a polypeptide comprising an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said sequence variant has aminopeptidase activity and is encoded by a nucleotide sequence having at least about 85% sequence identity to SEQ ID NO:2 as calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4;

- 20 (b) the amino acid sequence of a sequence variant of the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said sequence variant has aminopeptidase activity and is encoded by a nucleotide sequence having at least about 85% sequence identity to SEQ ID NO:2 as calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4;

- 25 (c) the amino acid sequence of a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said sequence variant has aminopeptidase activity and is encoded by a nucleotide sequence having at least about 90% sequence identity to SEQ ID NO:2 as calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4;

- 30 (d) the amino acid sequence of a sequence variant of the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said sequence variant has aminopeptidase activity and is encoded by a nucleotide sequence having at least about 90% sequence identity to SEQ ID

NO:2 as calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4;

(e) the amino acid sequence of a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said sequence variant has aminopeptidase activity and is encoded by a nucleotide sequence having at least about 95% sequence identity to SEQ ID NO:2 as calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4;

(f) the amino acid sequence of a sequence variant of the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said sequence variant has aminopeptidase activity and is encoded by a nucleotide sequence having at least about 95% sequence identity to SEQ ID NO:2 as calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4;

(g) the amino acid sequence of a fragment of the amino acid sequence set forth in SEQ ID NO:1, wherein said amino acid sequence has aminopeptidase activity and is encoded by nucleotide sequence comprising at least 500 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:2; and

(h) the amino acid sequence of a fragment of the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said fragment has aminopeptidase activity and is encoded by a nucleotide sequence comprising at least 500 contiguous nucleotides of the nucleotide sequence of the cDNA insert of the plasmid deposited with ATCC as Patent Deposit No. PTA-2811;

said method comprising introducing a nucleotide sequence encoding the polypeptide into a host cell, and culturing the host cell under conditions in which the polypeptide is expressed from the nucleotide sequence.

7. The method of claim 6, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said variant has aminopeptidase activity and

is encoded by a nucleotide sequence having at least about 85% sequence identity to SEQ ID NO:2 as calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4; and

- (b) the amino acid sequence of a sequence variant of the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said sequence variant has aminopeptidase activity and is encoded by a nucleotide sequence having at least about 85% sequence identity to SEQ ID NO:2 as calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4.

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8. The method of claim 7, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said variant has aminopeptidase activity and is encoded by a nucleotide sequence having at least about 90% sequence identity to SEQ ID NO:2 as calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4; and

- (b) the amino acid sequence of a sequence variant of the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said sequence variant has aminopeptidase activity and is encoded by a nucleotide sequence having at least about 90% sequence identity to SEQ ID NO:2 as calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4.

25 9. The method of claim 6, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said variant has aminopeptidase activity and is encoded by a nucleotide sequence having at least about 95% sequence identity to SEQ ID NO:2 as calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4; and

(b) the amino acid sequence of a sequence variant of the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said sequence variant has aminopeptidase activity and is encoded by a nucleotide sequence having at least about 95% sequence identity to SEQ ID NO:2 as calculated using the GAP algorithm with a gap weight of 12 and a length weight of 4.

10. The method of claim 6, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of:

10 (a) the amino acid sequence of a fragment of the amino acid sequence set forth in SEQ ID NO:1, wherein said amino acid sequence has aminopeptidase activity and is encoded by nucleotide sequence comprising at least 500 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:2; and

(b) the amino acid sequence of a fragment of the amino acid sequence encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said fragment has aminopeptidase activity and is encoded by a nucleotide sequence comprising at least 500 contiguous nucleotides of the nucleotide sequence of the cDNA insert of the plasmid deposited with ATCC as Patent Deposit No. PTA-2811.

11. A method for detecting the presence of a nucleic acid molecule in a sample, said method comprising contacting the sample with a nucleic acid probe comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence encoding a fragment of the amino acid sequence set forth in SEQ ID NO:1, wherein said nucleotide sequence comprises at least 500 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:2;

(b) a nucleotide sequence encoding a fragment of the amino acid sequence encoded by the cDNA insert contained in the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said nucleotide sequence comprises at least 500 contiguous nucleotides of the nucleotide sequence of the cDNA insert of the plasmid deposited with ATCC as Patent Deposit No. PTA-2811;

(c) a nucleotide sequence encoding a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said nucleotide sequence has at least about 85% sequence identity with the nucleotide sequence set forth in SEQ ID NO:2, and said sequence variant has aminopeptidase activity;

5 (d) a nucleotide sequence encoding a sequence variant of the amino acid sequenced encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said nucleotide sequence has at least about 85% sequence identity with the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, and said sequence variant has aminopeptidase activity;

10 (e) a nucleotide sequence encoding a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said nucleotide sequence has at least about 90% sequence identity with the nucleotide sequence set forth in SEQ ID NO:2, and said sequence variant has aminopeptidase activity;

(f) a nucleotide sequence encoding a sequence variant of the amino acid sequenced encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said nucleotide sequence has at least about 90% sequence identity with the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, and said sequence variant has aminopeptidase activity;

15 (g) a nucleotide sequence encoding a sequence variant of the amino acid sequence set forth in SEQ ID NO:1, wherein said nucleotide sequence has at least about 95% sequence identity with the nucleotide sequence set forth in SEQ ID NO:2, and said sequence variant has aminopeptidase activity;

(h) a nucleotide sequence encoding a sequence variant of the amino acid sequenced encoded by the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, wherein said nucleotide sequence has at least about 95% sequence identity with the cDNA insert of the plasmid deposited with the ATCC as Patent Deposit No. PTA-2811, and said sequence variant has aminopeptidase activity; and

25 (i) a nucleotide sequence complementary to at least one of the
30 nucleotide sequences in (a), (b), (c), (d), (e), (f), (g), or (h);

and determining whether the nucleic acid probe binds to a nucleic acid molecule in the sample.

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